

FIG. 1A

```

ccacgcgtcc ggagcgcccc agggagctca gagcttgtgc aagcgtggca gcaggaggag 60
gccagtcccc agcttttagtc caccgctcct ctcccttgag cccctgaatt gcattttgca 120
gtagctcgaa ggagaaaaaa gtagaag atg gat ggc atg aaa tac atc att tcc 174
      Met Asp Gly Met Lys Tyr Ile Ile Ser
              1              5

tta ttt ttc atc ttt gtt ttc cta gaa gga agc aaa aca gaa caa gta 222
Leu Phe Phe Ile Phe Val Phe Leu Glu Gly Ser Lys Thr Glu Gln Val
      10              15              20              25

aaa cac tca gac aca tat tgc gtg ttt caa gac aag aag tat aga gtg 270
Lys His Ser Asp Thr Tyr Cys Val Phe Gln Asp Lys Lys Tyr Arg Val
              30              35              40

ggg gag aaa tgg cat ccc tac ctg gaa ccg tat gga ctg gtt tac tgt 318
Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys
              45              50              55

gtg aac tgc atc tgc tct gag aat ggg aat gtg ctt tgc agc cga gtc 366
Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val
              60              65              70

aga tgt cca agt ctt cat tgc ctt tca ccc gtg cat att cct cat ctc 414
Arg Cys Pro Ser Leu His Cys Leu Ser Pro Val His Ile Pro His Leu
              75              80              85

tgt tgc ccc cgc tgc cca gac tcc tta cca cca gtg aac aat aag gtg 462
Cys Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val
              90              95              100              105

acc agc aag tca tgc gaa tac aat gga acc act tac caa cat gga gaa 510
Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu
              110              115              120

ctg ttc ata gct gaa ggg ctc ttt cag aac cgg caa ccc aat cag tgc 558
Leu Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys
              125              130              135

agt cag tgt agc tgc tcg gag ggg aat gta tac tgt ggt ctc aag act 606
Ser Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr
              140              145              150

tgc ccc aaa ctg acc tgt gca ttc cca gtc tct gtt cca gat tct tgc 654
Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys
              155              160              165

tgc cga gta tgc aga ggg gat gca gaa tta tcg tgg gaa cat gcg gat 702
Cys Arg Val Cys Arg Gly Asp Ala Glu Leu Ser Trp Glu His Ala Asp
      170              175              180              185

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CCAGGAGGAG

[illegible]

ggt gat atc ttc cgg caa cct gcc aac aga gaa gca aga cat tct tac	750
Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr	
190 195 200	
ctc cgt tcc ccc tac gat cct cca cca aac aga caa gct gga ggt ctt	798
Leu Arg Ser Pro Tyr Asp Pro Pro Pro Asn Arg Gln Ala Gly Gly Leu	
205 210 215	
ccc cgc ttt cct ggg agc aga agt cac cgg gga gct gtt ata gat tcc	846
Pro Arg Phe Pro Gly Ser Arg Ser His Arg Gly Ala Val Ile Asp Ser	
220 225 230	
cag caa gca tcc ggg acc atc gtg cag att gtc atc aat aac aag cac	894
Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His	
235 240 245	
aaa cat gga caa gtg tgt gtt tcc aat gga aag acc tac tct cat gga	942
Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly	
250 255 260 265	
gag tcc tgg cac cca aat cta cga gca ttt ggc att gtg gaa tgt gta	990
Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val	
270 275 280	
cta tgc act tgt aat gtc acc aag caa gaa tgt aag aaa atc cac tgc	1038
Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys	
285 290 295	
ccc aat cga tac ccc tgc aag tat cct caa aaa ata gat gga aag tgc	1086
Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys	
300 305 310	
tgc aag gtg tgc cca ggt aaa aag gca aaa ggt gca ttg gct gga ggc	1134
Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Gly Ala Leu Ala Gly Gly	
315 320 325	
cct gcc ttt ggt tgaatgagat tcacacatag tcctattcag tcttctttgt	1186
Pro Ala Phe Gly	
330	
tcatcaaaac tataaatgac ctgtcttata gttctaacga taatagttct agcaagaatg	1246
aacttcatcc tttcgtcttc tgagacactg atgggttgctt tgaaggaatt aactactcag	1306
agtttctttt gtctacaatg tcaaacacat gccaaagtgc ttatcttggt cttgcttttc	1366
taaattagag agtttacgtt atcactgttt tagaaaaagt cacaccttc atgggtttaa	1426
tcaccaactc acttcaagac ataatccagt actcttttca gatgagatat aaatgagtta	1486
cagtggagag aaattagatt ctgatccaaa tgcatacaat ccacaagtat cttaccccat	1546
gtgaacattt taaagtttat tactgtgttc cacattgcta ttttaatttg caatttcttt	1606

FIG. 1C

ttaaattttc	tgagatat	tgtatgtata	tacttatggg	gtacagtatg	ttaattcaat	1666
acaaatatac	aagggtataat	tgtcaaatca	gggtaattat	cattctctct	cctctgattt	1726
tatccctaga	ctcttctagt	catttttaaaa	tttatcatca	attgggtttt	tgatatggta	1786
actccactgt	gctaaagaaa	ccattcattc	taatggcatt	ttaggatcta	ctatctaacc	1846
tctatctccc	cttctgtt					1864

[illegible]

FIG. 2A

ccacgcgtcc gagcgcccca gggagctcag agcgtgtgca agcgtggcag aaggaagagg 60
ccagtgccca gcttttagccc accagtcccta ggagtctctg agctgcattt tgcagtagct 120
caaaggagaa gagagtggaa a atg gaa ggc ata aaa tat atc gcc tcc ttg 171
Met Glu Gly Ile Lys Tyr Ile Ala Ser Leu
1 5 10
gtt ttc ttc ttt gtt ttc ctg gaa gca agc aaa aca gag cca gta aaa 219
Val Phe Phe Phe Val Phe Leu Glu Ala Ser Lys Thr Glu Pro Val Lys
15 20 25
cac tca gag aca tat tgc atg ttt caa gac aag aag tat aga gtt ggt 267
His Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly
30 35 40
gag aaa tgg cat ccc tac ctg gaa cca tat gga ctg gtt tac tgt gtg 315
Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val
45 50 55
aac tgc atc tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga 363
Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg
60 65 70
tgt cca act ctt cat tgc ctt tca ccc gtg cat att cct cat ctg tgt 411
Cys Pro Thr Leu His Cys Leu Ser Pro Val His Ile Pro His Leu Cys
75 80 85 90
tgc ccc cgt tgc cca gac tcc tta cca ccg atg aac aat aag gtg acc 459
Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Met Asn Asn Lys Val Thr
95 100 105
agc aag tcc tgc gaa tac aat ggg acc acc tac caa cac gga gag ctc 507
Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu
110 115 120
ttc ata gct gaa ggg ctc ttt cag aac cgg cag ccc aat cag tgc agt 555
Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser
125 130 135
cag tgc agc tgc tgc gag ggg aat gtg tat tgt ggt ctc aag act tgc 603
Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys
140 145 150
ccc aaa ctg acc tgt gca ttc cca gtc tct gtt cca gat tcc tgc tgc 651
Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys
155 160 165 170
cga gta tgc aga ggg gat gga gaa tta tca tgg gaa cat tct gat gct 699
Arg Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Ala
175 180 185

U18621-512626

FIG. 2B

gat atc ttc cgg caa cct gcc aac aga gaa gca aga cat tct tac ctc	747
Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr Leu	
190 195 200	
cgt tcc ccc tac gat cct cca cca agc aga caa gct gga ggt ctt cct	795
Arg Ser Pro Tyr Asp Pro Pro Ser Arg Gln Ala Gly Gly Leu Pro	
205 210 215	
cgc ttt gct ggg agc aga agt cac cgg gga gct gtc att gat tct cag	843
Arg Phe Ala Gly Ser Arg Ser His Arg Gly Ala Val Ile Asp Ser Gln	
220 225 230	
caa gca tca ggg acc atc gtg cag atc gtc atc aat aac aag cac aaa	891
Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys	
235 240 245 250	
cat gga caa gtg tgt gtt tcc aat gga aag acc tat tct cac gga gaa	939
His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu	
255 260 265	
tcc tgg cat tca aat cta cga gct ttt ggc att gtg gaa tgt gtt cta	987
Ser Trp His Ser Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu	
270 275 280	
tgc act tgt aat gtc acc aag caa gaa tgt aag aaa atc cac tgc ccc	1035
Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys Pro	
285 290 295	
aat cga tac ccc tgc aag tat cct caa aaa tta gat gga aag tgc tgc	1083
Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Leu Asp Gly Lys Cys Cys	
300 305 310	
aag gtg tgc cca gaa gaa cct cca agt caa aac ttt gac agc aaa ggt	1131
Lys Val Cys Pro Glu Glu Pro Pro Ser Gln Asn Phe Asp Ser Lys Gly	
315 320 325 330	
tcc ttt tgt gga gaa gaa acc atg cct gta tat gag gct gtg ctc gtg	1179
Ser Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu Ala Val Leu Val	
335 340 345	
gag gat gga gag aca gcc aga aaa gta gca ctg gag acc gag aaa cca	1227
Glu Asp Gly Glu Thr Ala Arg Lys Val Ala Leu Glu Thr Glu Lys Pro	
350 355 360	
cct caa gta gta ggt tca cgt ttg gac tat tcg aaa ggg cat tct cca	1275
Pro Gln Val Val Gly Ser Arg Leu Asp Tyr Ser Lys Gly His Ser Pro	
365 370 375	
gca ctt cca cat tgagaagatt tccaaggaga tgtttgggga gctccatcat	1327
Ala Leu Pro His	
380	
ttcaagctgg tgactcgaac caccatgaac cagtggaaga tcttcgctga aggagaagct	1387

GenBank: 513146.1

FIG. 2C

cagctcagcc agatgtgctc aagtcgggtg tgcagaacag aactggaaga tttggtccag 1447
 gttttgtacc tggagagacc tgaaaaggac cactgttaga caaaacagtc aggattgaat 1507
 agtatcaatc aaggaaaccc aagctgcagc tggactgccg gcttacttta cttaaagtcaa 1567
 cagtgtcca aaaccccaaa gtcaacctca gtcaaattat ccagtcacag cacaccttgt 1627
 tcctctatgt gcagcgggtg gccagccctc aaacatctcc tgtaaagaga atagaggagt 1687
 ctttaatggt ttctgggggt ggggggagaa gggataggac tttgtggtac agctctat 1747
 tctctgagaa tcacatttat ttgcagggtta aagtagaaaa gaaaaccact ttttagggat 1807
 tctatgtaga aagtcacaag agagagagag agagaaattg ctgagtttga gttggatcat 1867
 gccaaacaaa tttgtgtgaa atactttttg aatgttcaag tgtcttccct actttaaaaa 1927
 tgttattcag ttggtggttg aacagtcagg tgattatgga gcacatacct ataatatgtg 1987
 gagacctggg ttctagtctc agaactgaca aaaaaatttc tatcctcata tctcacatgc 2047
 acacacacac acacacacac acacacacac acacacacac acacacacac acagcacacg 2107
 aaactgcatt tctttctggc tcctaaacac ctttgtggtt gttcgtatcc agggaaacaa 2167
 actaaaaatg tatgcaaaaa actctgcctt caagcctttg aggcagggtg taagaaatca 2227
 gccatagtct tagagtgaag aatgccattt gtgggtcttg tttccttcga agtactaaat 2287
 acattttgcc tagtaatatc acttctcttt tcttatctgg caccctcatt aggaaggtag 2347
 aatttgagaa actcatcaga aactaaattt attccaaaca aaatgacaat agaagaatat 2407
 aactgataaa aaataaaata gtccattttt tgttttggtt ttacagctat aaatctaact 2467
 gattaatagg ctaatgatgc tactaattt tcttgaggca atagtcacct aggcagacac 2527
 tttagggtga cacttttatt ctaaaagcct ttttaagggt aatttcctac tttgattaca 2587
 ggagttgaaa tgtaactttt caaaaaggct caatccttac aagcttctca acatcagttc 2647
 ttctgttaag tgctactggt cattcacaga gctgagaatt ctggcaaaga tctttgtccc 2707
 aacccttctt aatatccttg ccttattctt gagcatgggt tgcagcaggg attgtgacag 2767
 cactacttct aaaatgttca tttgcagccc agtgcctcaa catcaatttt ccttctgag 2827
 gcttggtctt agaaatcacc ttttgaaaaa actataacta ttccctagca aagatcatag 2887
 gttcactgga tctgtccatc tgccgagcat gaatgaactc acatgagtac taagaaatgt 2947
 gaagatcaag aaattctata tttccctc taagtgagaa aacatgatag gaaaaagtat 3007

GenBank: F01466

FIG. 2D

gaagagtctg gtctttacta gaacctgaca gagaagggaa ggctttgggg ccagggttc 3067
atgagacaaa cttcctgcc aaccaattaca cattctccca agaagagaag catagggcgt 3127
cctgggctgc aaagacactg aacattattg aagatgtgat ggggcaatgc caaccctctg 3187
ctgcttcctt cttggaggaa aactatttc cagagtgcgg agatcaatca caggctcctga 3247
aggaaagtgg tgattcctgt gctagacgat tcacccgcag ggaagggtgg gattcccgtg 3307
ctagatgatt cactcacaaa ccttcccgc cagggtgttct ctgaaagctt agcctcaagg 3367
gaacacctaa agagctcccc tacctacata aaccctgcc tccaagtgt ggaactcacc 3427
tttctaaagc gctgtgggaa gcaggaactg ggcattctgt ctaagtcaat gtagaatttc 3487
tccagcgttt taatgctggg tagaatatag agcatagggg aaagggggcca aactgcctat 3547
agttagtaga gaaaaatgaa tgtggttctt ttgtgcattt atgtgtatca taaacacttg 3607
ggaaagcaaa aaccataagc accattttgc aactttatcc attttccagt tagctcatgt 3667
aaacgagcac gaataacaaa acagtattac tctttcgcac ttctcacagg acatgtaccc 3727
aaatacggta cttatttatg tagtcactgt gtttcaggac ttttacgtta ataaaatttt 3787
tattttaaatt tttaaaaaaa aaaaaaaaaa aaaaaaaaaa 3827

CGCGTGGG

FIG. 3A

tagccagacc	tccgacgaga	gcgccccggg	gagctcggag	cgcgtgcacg	cgtggcagac	60
ggagaaggcc	agtgccccagc	ttgaagggtc	tgccaccttt	tgcagtggtc	caaatgagaa	120
aaaagtggaa	a atg gga ggc atg aaa tac atc ttt tgc ttg ttg ttc ttt	170				
	<u>Met Gly Gly Met Lys Tyr Ile Phe Ser Leu Leu Phe Phe</u>					
	<u>1 5 10</u>					
ctt ttg cta gaa gga ggc aaa aca gag caa gta aaa cat tca gag aca	218					
Leu Leu Leu Glu Gly Gly Lys Thr						
<u>15 20 25</u>						
tat tgc atg ttt caa gac aag aag tac aga gtg ggt gag aga tgg cat	266					
Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Arg Trp His						
<u>30 35 40 45</u>						
cct tac ctg gaa cct tat ggg ttg gtt tac tgc gtg aac tgc atc tgc	314					
Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys						
<u>50 55 60</u>						
tca gag aat ggg aat gtg ctt tgc agc cga gtc aga tgt cca aat gtt	362					
Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Asn Val						
<u>65 70 75</u>						
cat tgc ctt tct cct gtg cat att cct cat ctg tgc tgc cct cgc tgc	410					
His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys						
<u>80 85 90</u>						
cca gaa gac tcc tta ccc cca gtg aac aat aag gtg acc agc aag tct	458					
Pro Glu Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser						
<u>95 100 105</u>						
tgc gag tac aat ggg aca act tac caa cat gga gag ctg ttc gta gct	506					
Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Val Ala						
<u>110 115 120 125</u>						
gaa ggg ctc ttt cag aat cgg caa ccc aat caa tgc acc cag tgc agc	554					
Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln Cys Ser						
<u>130 135 140</u>						
tgt tgc gag gga aac gtg tat tgt ggt ctc aag act tgc ccc aaa tta	602					
Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu						
<u>145 150 155</u>						
acc tgt gcc ttc cca gtc tct gtt cca gat tcc tgc tgc cgg gta tgc	650					
Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys						
<u>160 165 170</u>						
aga gga gat gga gaa ctg tca tgg gaa cat tct gat ggt gat atc ttc	698					
Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp Ile Phe						
<u>175 180 185</u>						

003217-9161260

FIG. 3C

[illegible]

FIG. 4A

atg	gga	ggc	atg	aaa	tac	atc	ttt	tcg	ttg	ttc	ttt	ctt	ttg	cta		48	
Met	Gly	Gly	Met	Lys	Tyr	Ile	Phe	Ser	Leu	Leu	Phe	Phe	Leu	Leu	Leu		
1			5			10			15								
gaa	gga	ggc	aaa	aca	gag	caa	gta	aaa	cat	tca	gag	aca	tat	tgc	atg	96	
Glu	Gly	Gly	Lys	Thr	Glu	Gln	Val	Lys	His	Ser	Glu	Thr	Tyr	Cys	Met		
20				25				30									
ttt	caa	gac	aag	aag	tac	aga	gtg	ggg	gag	aga	tgg	cat	cct	tac	ctg	144	
Phe	Gln	Asp	Lys	Lys	Tyr	Arg	Val	Gly	Glu	Arg	Trp	His	Pro	Tyr	Leu		
35			40			45											
gaa	cct	tat	ggg	ttg	gtt	tac	tgc	gtg	aac	tgc	atc	tgc	tca	gag	aat	192	
Glu	Pro	Tyr	Gly	Leu	Val	Tyr	Cys	Val	Asn	Cys	Ile	Cys	Ser	Glu	Asn		
50			55			60											
ggg	aat	gtg	ctt	tgc	agc	cga	gtc	aga	tgt	cca	aat	gtt	cat	tgc	ctt	240	
Gly	Asn	Val	Leu	Cys	Ser	Arg	Val	Arg	Cys	Pro	Asn	Val	His	Cys	Leu		
65		70			75			80									
tct	cct	gtg	cat	att	cct	cat	ctg	tgc	tgc	cct	cgc	tgc	cca	gaa	gac	288	
Ser	Pro	Val	His	Ile	Pro	His	Leu	Cys	Cys	Pro	Arg	Cys	Pro	Glu	Asp		
85				90				95									
tcc	tta	ccc	cca	gtg	aac	aat	aag	gtg	acc	agc	aag	tct	tgc	gag	tac	336	
Ser	Leu	Pro	Pro	Val	Asn	Asn	Lys	Val	Thr	Ser	Lys	Ser	Cys	Glu	Tyr		
100			105			110											
aat	ggg	aca	act	tac	caa	cat	gga	gag	ctg	ttc	gta	gct	gaa	ggg	ctc	384	
Asn	Gly	Thr	Thr	Tyr	Gln	His	Gly	Glu	Leu	Phe	Val	Ala	Glu	Gly	Leu		
115			120			125											
ttt	cag	aat	cgg	caa	ccc	aat	caa	tgc	acc	cag	tgc	agc	tgt	tcg	gag	432	
Phe	Gln	Asn	Arg	Gln	Pro	Asn	Gln	Cys	Thr	Gln	Cys	Ser	Cys	Ser	Glu		
130			135			140											
gga	aac	gtg	tat	tgt	ggg	ctc	aag	act	tgc	ccc	aaa	tta	acc	tgt	gcc	480	
Gly	Asn	Val	Tyr	Cys	Gly	Leu	Lys	Thr	Cys	Pro	Lys	Leu	Thr	Cys	Ala		
145		150			155			160									
ttc	cca	gtc	tct	gtt	cca	gat	tcc	tgc	tgc	cgg	gta	tgc	aga	gga	gat	528	
Phe	Pro	Val	Ser	Val	Pro	Asp	Ser	Cys	Cys	Arg	Val	Cys	Arg	Gly	Asp		
165				170				175									
gga	gaa	ctg	tca	tgg	gaa	cat	tct	gat	ggg	gat	atc	ttc	cgg	caa	cct	576	
Gly	Glu	Leu	Ser	Trp	Glu	His	Ser	Asp	Gly	Asp	Ile	Phe	Arg	Gln	Pro		
180			185			190											
gcc	aac	aga	gaa	gca	aga	cat	tct	tac	cac	cgc	tct	cac	tat	gat	cct	624	
Ala	Asn	Arg	Glu	Ala	Arg	His	Ser	Tyr	His	Arg	Ser	His	Tyr	Asp	Pro		
195			200			205											

FIG. 4B

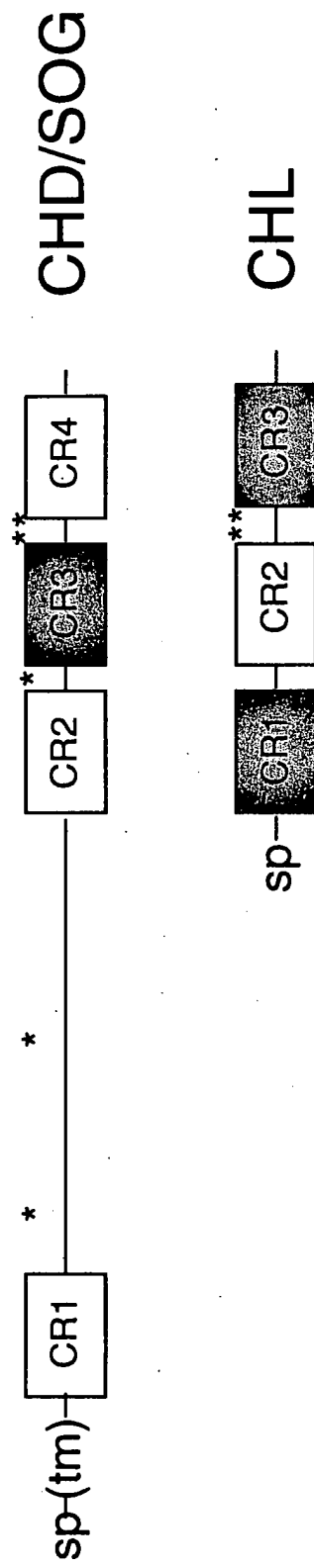
cca cca agc cga cag gct gga ggt ctg tcc cgc ttt cct ggg gcc aga	672
Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg Phe Pro Gly Ala Arg	
210 215 220	
agt cac cgg gga gct ctt atg gat tcc cag caa gca tca gga acc att	720
Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln Ala Ser Gly Thr Ile	
225 230 235 240	
gtg caa att gtc atc aat aac aaa cac aag cat gga caa gtg tgt gtt	768
Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val	
245 250 255	
tcc aat gga aag acc tat tct cat ggc gag tcc tgg cac cca aac ctc	816
Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu	
260 265 270	
cgg gca ttt ggc att gtg gag tgt gtg cta tgt act tgt aat gtc acc	864
Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr	
275 280 285	
aag caa gag tgt aag aaa atc cac tgc ccc aat cga tac ccc tgc aag	912
Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys	
290 295 300	
tat cct caa aaa ata gac gga aag tgc tgc aag gtg tgt cca gaa gaa	960
Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Glu Glu	
305 310 315 320	
ctt cca ggc caa agc ttt gac aat aaa ggc tac ttc tgc ggg gaa gaa	1008
Leu Pro Gly Gln Ser Phe Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu	
325 330 335	
acg atg cct gtg tat gag tct gta ttc atg gag gat ggg gag aca acc	1056
Thr Met Pro Val Tyr Glu Ser Val Phe Met Glu Asp Gly Glu Thr Thr	
340 345 350	
aga aaa ata gca ctg gag act gag aga cca cct cag gta gag gtc cac	1104
Arg Lys Ile Ala Leu Glu Thr Glu Arg Pro Pro Gln Val Glu Val His	
355 360 365	
gtt tgg act att cga aag ggc att ctc cag cac ttc cat att gag aag	1152
Val Trp Thr Ile Arg Lys Gly Ile Leu Gln His Phe His Ile Glu Lys	
370 375 380	
atc tcc aag agg atg ttt gag gag ctt cct cac ttc aag ctg gtg acc	1200
Ile Ser Lys Arg Met Phe Glu Glu Leu Pro His Phe Lys Leu Val Thr	
385 390 395 400	
aga aca acc ctg agc cag tgg aag atc ttc acc gaa gga gaa gct cag	1248
Arg Thr Thr Leu Ser Gln Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln	
405 410 415	

GenBank: 51542460

tta gtc aag gtt ttg tac ctg gag aga tct gaa aag ggc cac tgt	1341
Leu Val Lys Val Leu Tyr Leu Glu Arg Ser Glu Lys Gly His Cys	
435 440 445	

[illegible]

FIG. 5



CR: pro-collagen repeat

sp: signal peptide

tm: transmembrane domain (only in *Drosophila sog*)

*: possible BMP1 cleavage site (A/GD sequence)

FIG. 6A

	1					50
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchordin	MPSLPAPPAP	RLLLGLLLLG	SRPASGTGPE	PPALPIRSEK	EPLPVRGAAG	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
	51					100
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchordin	CSFGGKVYAL	DETHWPDLGE	PFGVMRCVLC	ACEAPQWARR	GRGPGRVSCK	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
	101					150
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchordin	NIKQQCPTLA	CRQPRQLPGH	CCQTC PQERS	NLDPQPAGLV	FEYPRDPEHR	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	~~~~~	~~~~~QVAAGH	CCQTC PQERS	SSERQPSGLS	FEYPRDPEHR	
	151					200
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchordin	SYSDRGEPGV	GERTRADGHT	DFVALLTGPR	SQAVARARVS	LLRSSLRFSV	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	SYSDRGEPGA	EERARGDGHT	DFVALLTGPR	SQAVARARAS	LLRSSLRFSI	
	201					250
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchordin	SYQRLDRPSR	VRFTDPTGNI	LFEHPATPTQ	DGLVCGVWRA	VPRLSVRLLR	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	SYRRLDRPTR	IRFSDPNGSV	LFEHPAAPTQ	DGLVCGVWRA	VPRLSLRLLR	
	251					300
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Mchordin	AEQLRVALVT	STHPSGEVWG	PLIWQGALAA	ETFSAILTLE	DPLQRGVGGI	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	AEQLHVALVT	LTHPSGEVWG	PLIRHRALAA	ETFSAILTLE	GPPQQGVGGI	

FIG. 6B

	301				350
Hchl	-----	-----	-----	-----	-----
Hchld5	-----	-----	-----	-----	-----
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	ALLTSLSDTED	SLHFLLLFRG	LL...GGLA	QAPLKLQILH	QGQLLRELQA
Rchordin	-----	-----	-----	-----	-----
Hchordin	TLLTSLSDTED	SLHFLLLFRG	LLEPRSGGLT	QVPLRLQILH	QGQLLRELQA
	351				400
Hchl	-----	-----	-----	-----	-----
Hchld5	-----	-----	-----	-----	-----
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	N TSAQEPGFA	EVLP SLTDQE	MDWLELGELQ	MVLEKAGGPE	LRISGYITTR
Rchordin	-----	-----	-----	-----	-----
Hchordin	NVSAQEPGFA	EVLP NLTVQE	MDWLVLGELQ	MALEWAGRPG	LRISGHIAAR
	401				450
Hchl	-----	-----	-----	-----	-----
Hchld5	-----	-----	-----	-----	-----
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	QSCDVLQSVL	CGADALIPVQ	TGAAGSASFI	LLGNGSLIYQ	VQVVG TGSEV
Rchordin	-----	-----	-----	-----	-----
Hchordin	KSCDVLQSVL	CGADALIPVQ	TGAAGSASLT	LLGNGSLIYQ
	451				500
Hchl	-----	-----	-----	-----	-----
Hchld5	-----	-----	-----	-----	-----
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	VAMTLETKPQ	RKNQRTVLCH	MAGLQPGGHM	AVGMCSGLGA	RGAHMLLQNE
Rchordin	-----	-----	-----	-----	-----
Hchordin	AVGICPGLGA	RGAHMLLQNE
	501				550
Hchl	-----	-----	-----	-----	-----
Hchld5	-----	-----	-----	-----	-----
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	LFLNVG TKDF	PDGELRGHVT	ALCYSGHSAR	YDRLPVPLAG	ALVLPPVRSQ
Rchordin	-----	-----	-----	-----	-----
Hchordin	LFLNVG TKDF	PDGELRGHVA	ALPYCGHSAR	HDTLPVPLAG	ALVLPPVKSQ
	551				600
Hchl	-----	-----	-----	-----	-----
Hchld5	-----	-----	-----	-----	-----
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	AAGHAWLSLD	THCHLHYEVL	LAGLGGSEQG	TVTAHLLGPP	GMPGPQRLLK
Rchordin	-----	-----	-----	-----	-----
Hchordin	AAGHAWLSLD	THCHLHYEVL	LAGLGGSEQG	TVTAHLLGPP	GTPGPRRLLK

000001 5160260

FIG. 6C

	601					650
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mchordin	GFYGSEAQGV	VKDLEPVLLR	HLAQGTASLL	ITTKSSPRGE	LRGQVHIASQ	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hchordin	GFYGSEAQGV	VKDLEPELLR	HLAKGMASLL	ITTKGSPRGE	LRGQVHIANQ	
	651					700
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mchordin	CEAGGLRLAS	EGVQMPLAPN	GEAATSPMLP	AGPGPEAPVP	AKHGSPGRPR	
Rchordin	---GGLRLAS	EGVRMSLAPN	GEAATSPMLP	AGPGPEAPVP	AKHGSSGRPR	
Hchordin	CEVGGLRLEA	AGAEGVRALG	APDPASAAPP	VVPGLPALAP	AKPGGPGRPR	
	701					750
Hchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Hchld5	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Rchl	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
Mchordin	DPNTCFFEGQ	QRPHGARWAP	NYDPLCSLCI	CQRRTVICDP	VVCPPPSCPH	
Rchordin	DPNTCFFEGQ	QRPHGARWAP	NYDPLCSLCT	CQRRTVICDP	VVCPPPRCSQ	
Hchordin	DPNTCFFEGQ	QRPHGARWAP	NYDPLCSLCT	CQRRTVICDP	VVCPPPSCPH	
	751					800
Hchl	----MGGMKY	IFSLLF.FLL	LEGGKTEQVK	HSETYCMFQD	KKYRVGERWH	
Hchld5	----MGGMKY	IFSLLF.FLL	LEGGKTEQVK	HSETYCMFQD	KKYRVGERWH	
Mchl	----MDGMKY	IISLFFIFVF	LEGSKTEQVK	HSDTYCVFQD	KKYRVGEKWH	
Rchl	----MEGIKY	IASLVFFFVF	LEASKTEPVK	HSETYCMFQD	KKYRVGEKWH	
Mchordin	PVQALDQCCP	VCPEKQSRSD	LPSLP.NLEP	GEGCYFDGDR	SWRAAGTRWH	
Rchordin	PVQALDQWCP	VCSEKQSRSD	LSSLP.NLEP	GEGCYFDGDR	SWRAAGTRWH	
Hchordin	PVQAPDQCCP	VCPEKQDVDR	LPGLPRSRDP	GEGCYFDGDR	SWRAAGTRWH	
	801					850
Hchl	PYLEPYGLVY	CVNCIC.SEN	GNVLCSSVRRC	PNVHCLSPVH	I.PHLCCPRC	
Hchld5	PYLEPYGLVY	CVNCIC.SEN	GNVLCSSVRRC	PNVHCLSPVH	I.PHLCCPRC	
Mchl	PYLEPYGLVY	CVNCIC.SEN	GNVLCSSVRRC	PSLHCLSPVH	I.PHLCCPRC	
Rchl	PYLEPYGLVY	CVNCIC.SEN	GNVLCSSVRRC	PTLHCLSPVH	I.PHLCCPRC	
Mchordin	PVPPPFGLIK	CAVCTCKGAT	GEVHCEKVQC	PRLACAQPVR	ANPTDCKQC	
Rchordin	PVPPPFGLIK	CGVCTCKGVN	GEVHSEKVQC	~~~~~	~~~~~	
Hchordin	PVPPPFGLIK	CAVCTCKGGT	GEVHCEKVQC	PRLACAQPVR	VNPTDCKQC	
	851					900
Hchl	PEDSLPPVNN	KVTSKSCEYN	GTTYQHSELF	VAEGLFQNRQ	PNQCTQCSCS	
Hchld5	PEDSLPPVNN	KVTSKSCEYN	GTTYQHSELF	VAEGLFQNRQ	PNQCTQCSCS	
Mchl	P.DSLPPVNN	KVTSKSCEYN	GTTYQHSELF	IAEGLFQNRQ	PNQCSQCSCS	
Rchl	P.DSLPPMNN	KVTSKSCEYN	GTTYQHSELF	IAEGLFQNRQ	PNQCSQCSCS	
Mchordin	PVGS..GTNA	KLGDPMQADG	PRGCRFAGQW	FPENQSWHPS	VPPFGEMSCI	
Rchordin	~~~~~	~~~~~	~~~~~	~~~~~	~~~~~	
Hchordin	PVGS..GAHP	QLGDPMQADG	PRGCRFAGQW	FPESQSWHPS	VPPFGEMSCI	

FIG. 6D

	901				950
Hchl	EGNVYCGLKT	CPKLTCAFPV	SVPDSCCRVC	RGDGELSWEH	SDGDIFRQPA
Hchld5	EGNVYCGLKT	CPKLTCAFPV	SVPDSCCRVC	RGDGELSWEH	SDGDIFRQPA
Mchl	EGNVYCGLKT	CPKLTCAFPV	SVPDSCCRVC	RGDAELSWEH	ADGDIFRQPA
Rchl	EGNVYCGLKT	CPKLTCAFPV	SVPDSCCRVC	RGDGELSWEH	SDADIFRQPA
Mchordin	TCRCGAGVPH	CERDDCSPPL	SCGSGKESRC	CSHCTAQR..	SSETRTLPEL
Rchordin	-----	-----	-----	-----	-----
Hchordin	TCRCGAGVPH	CERDDCSLPL	SCGSGKESRC	CSRCTAHRP	APETRTPDEL

	951				1000
Hchl	NREARHSYHR	SHYDPPPSRQ	AGGLSRFPGA	RSHRGALMDS	QQASGTIVQI
Hchld5	NREARHSYHR	SHYDPPPSRQ	AGGLSRFPGA	RSHRGALMDS	QQASGTIVQI
Mchl	NREARHSYLR	SPYDPPPNRQ	AGGLPRFPGS	RSHRGAVIDS	QQASGTIVQI
Rchl	NREARHSYLR	SPYDPPPSRQ	AGGLPRFAGS	RSHRGAVIDS	QQASGTIVQI
Mchordin	EKEAEHS---	-----	-----	-----	-----
Rchordin	-----	-----	-----	-----	-----
Hchordin	EKEAEGS---	-----	-----	-----	-----

	1001				1050
Hchl	VINNKHKHGQ	VCVSNGKTYS	HGESWHPNLR	AFGIVECVLC	TCNVTKQECK
Hchld5	VINNKHKHGQ	VCVSNGKTYS	HGESWHPNLR	AFGIVECVLC	TCNVTKQECK
Mchl	VINNKHKHGQ	VCVSNGKTYS	HGESWHPNLR	AFGIVECVLC	TCNVTKQECK
Rchl	VINNKHKHGQ	VCVSNGKTYS	HGESWHSNLR	AFGIVECVLC	TCNVTKQECK
Mchordin	-----	-----	-----	-----	-----
Rchordin	-----	-----	-----	-----	-----
Hchordin	-----	-----	-----	-----	-----

	1051				1100
Hchl	KIHCPNRYPC	KYPQKIDGKC	CKVCPGKKAK	EELPGQSFDN	KGYFCGEETM
Hchld5	KIHCPNRYPC	KYPQKIDGKC	CKVCP....	EELPGQSFDN	KGYFCGEETM
Mchl	KIHCPNRYPC	KYPQKIDGKC	CKVCPGKKAK	GALAGGPAFG	*-----
Rchl	KIHCPNRYPC	KYPQKLDGKC	CKVCP....	EEPPSQNFDS	KGSFCGEETM
Mchordin	-----	-----	-----	-----	-----
Rchordin	-----	-----	-----	-----	-----
Hchordin	-----	-----	-----	-----	-----

	1101				1150
Hchl	PVYESVFMED	GETTRKIALE	TERPPQVEVH	VWTIRKGILQ	HFHIEKISKR
Hchld5	PVYESVFMED	GETTRKIALE	TERPPQVEVH	VWTIRKGILQ	HFHIEKISKR
Mchl	-----	-----	-----	-----	-----
Rchl	PVYEAVLVED	GETARKVALE	TEKPPQVVGs	RLDYSKGHSP	ALPH*-----
Mchordin	-----	-----	-----	-----	-----
Rchordin	-----	-----	-----	-----	-----
Hchordin	-----	-----	-----	-----	-----

	1151				1200
Hchl	MFEELPHFKL	VTRTTLSQWK	IFTEGEAQIS	QMCSSRVCRT	ELEDLVKVLY
Hchld5	MFEELPHFKL	VTRTTLSQWK	IFTEGEAQIS	QMCSSRVCRT	ELEDLVKVLY
Mchl	-----	-----	-----	-----	-----
Rchl	-----	-----	-----	-----	-----
Mchordin	-----	-----	-----	-----	-----
Rchordin	-----	-----	-----	-----	-----
Hchordin	-----	-----	-----	-----	-----

DATE: 5/10/2000

	1201
Hchl	LERSEKGHC*
Hchld5	LERSEKGHC*
Mchl	~~~~~
Rchl	~~~~~
Mchordin	~~~~~
Rchordin	~~~~~
Hchordin	~~~~~

[illegible]

FIG. 7A

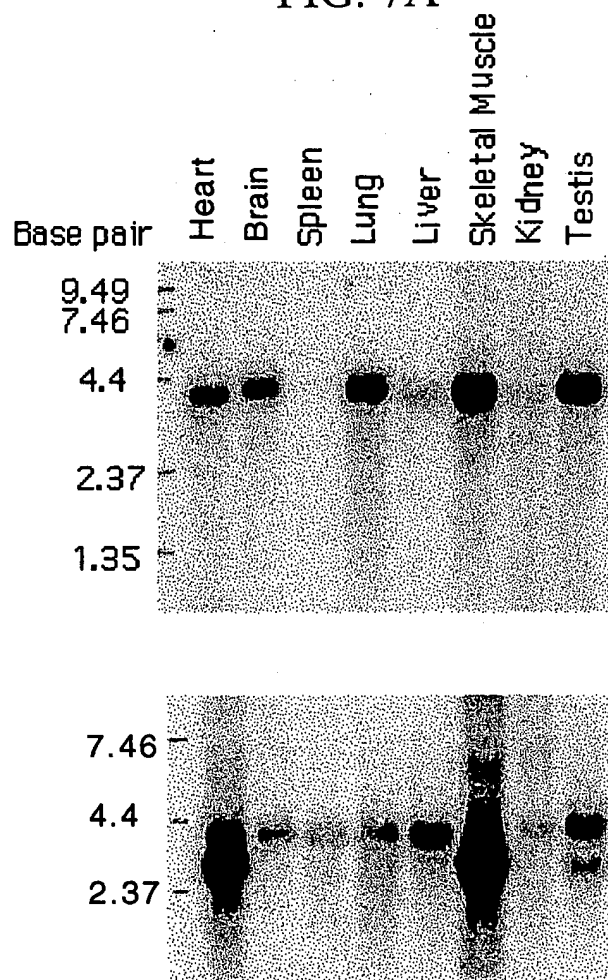
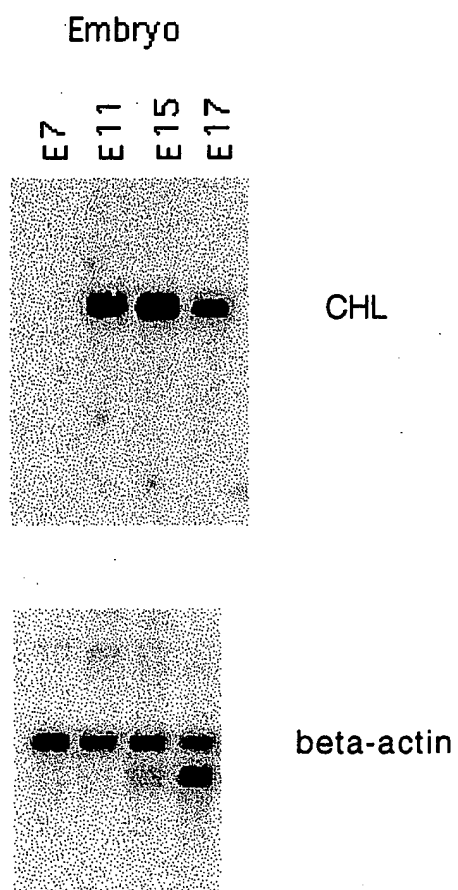


FIG. 7B



003245 FIG. 8

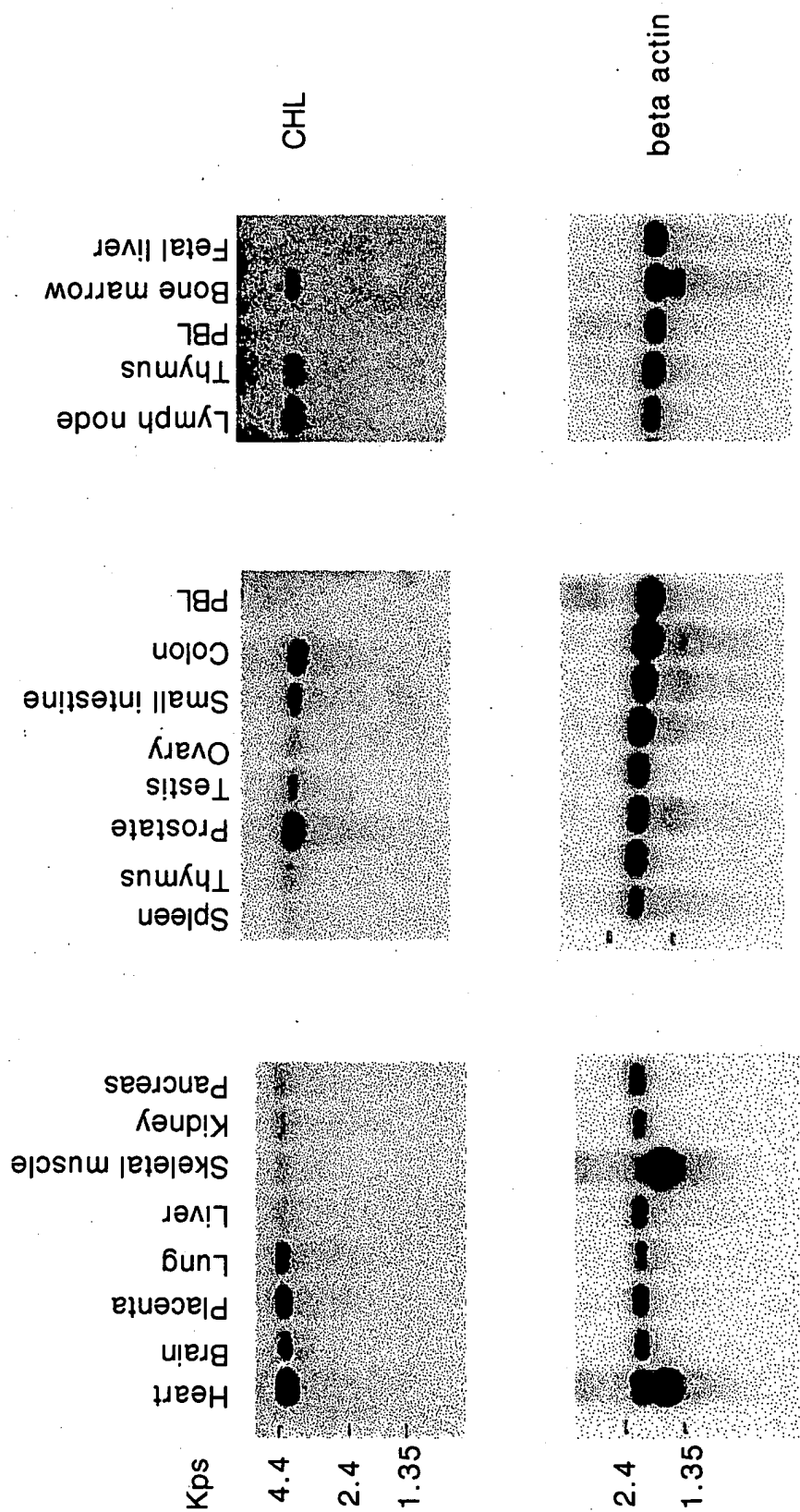
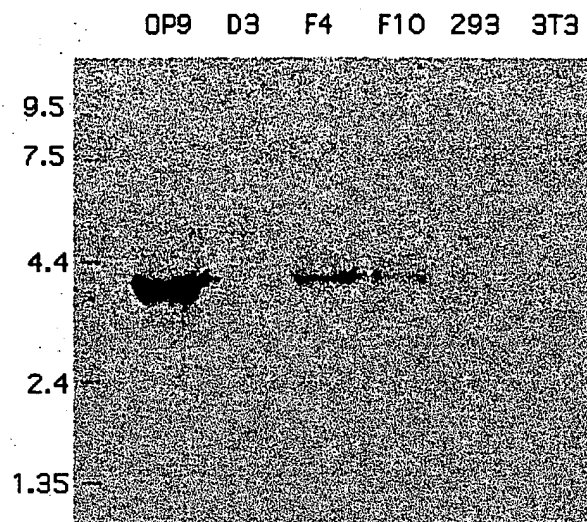
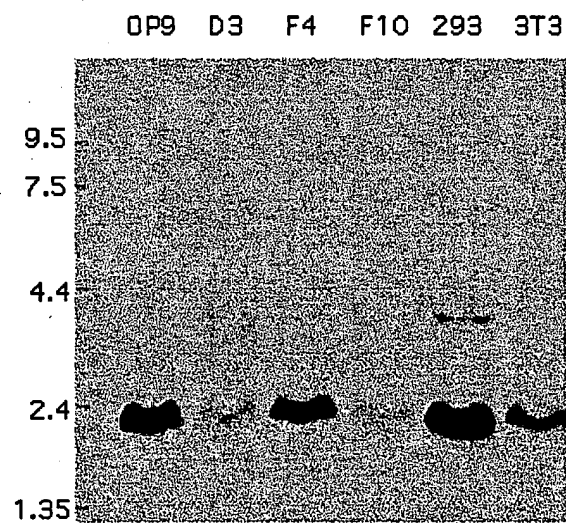


FIG. 9A



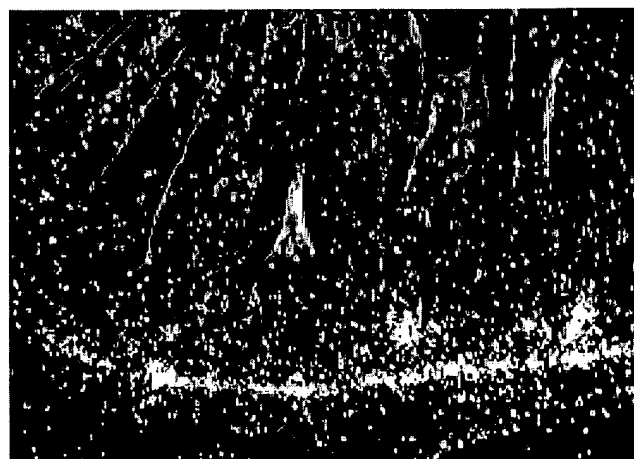
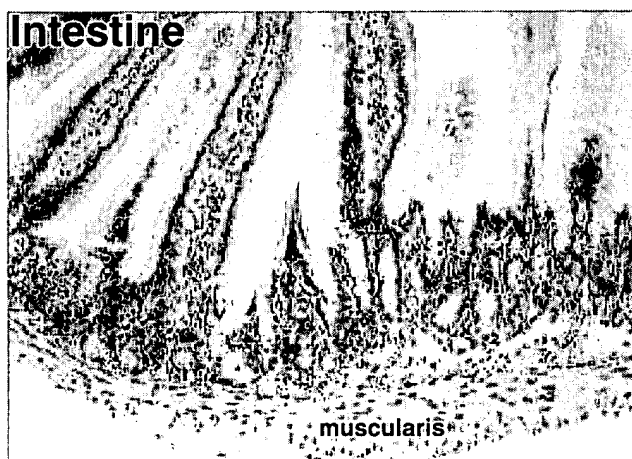
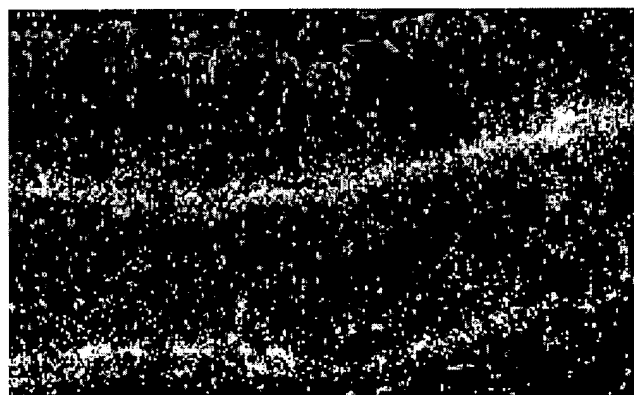
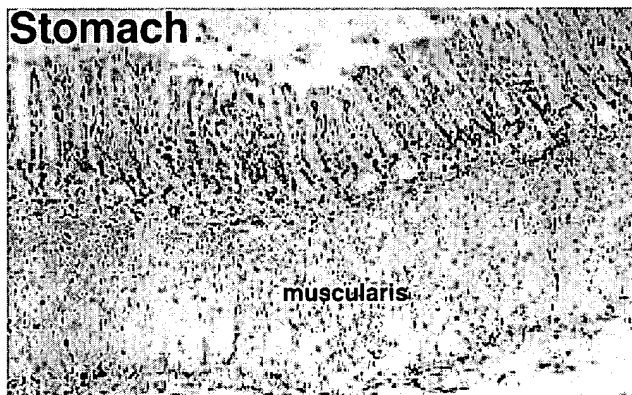
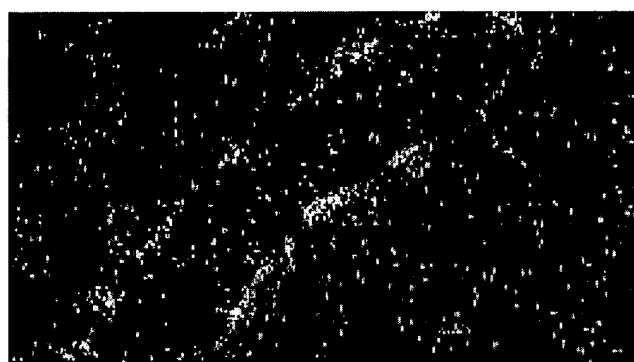
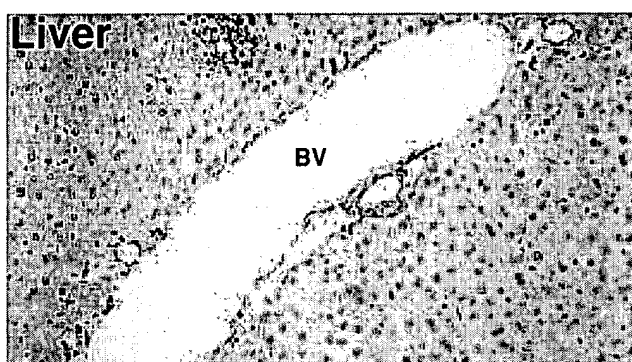
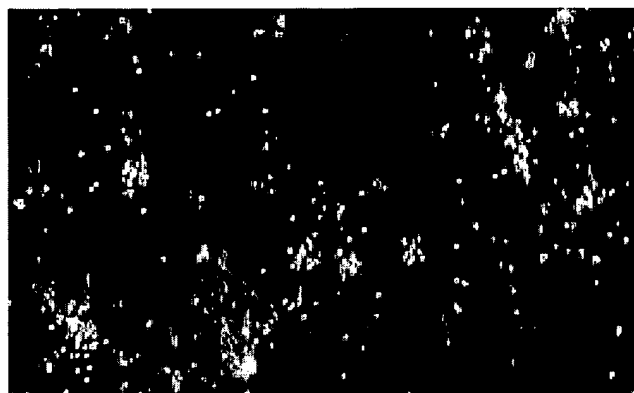
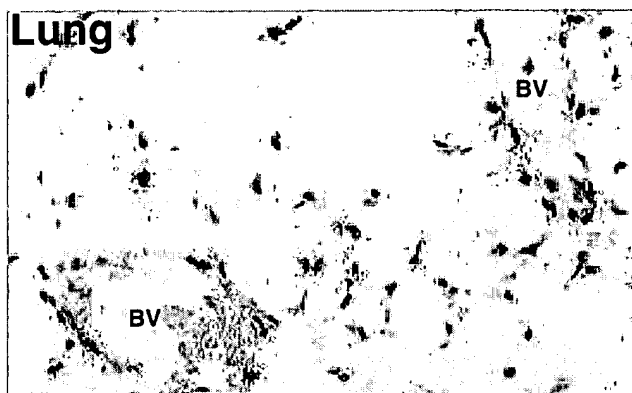
CHL expression

FIG. 9B



beta-actin control

FIG. 10



003211564260

FIG. 11

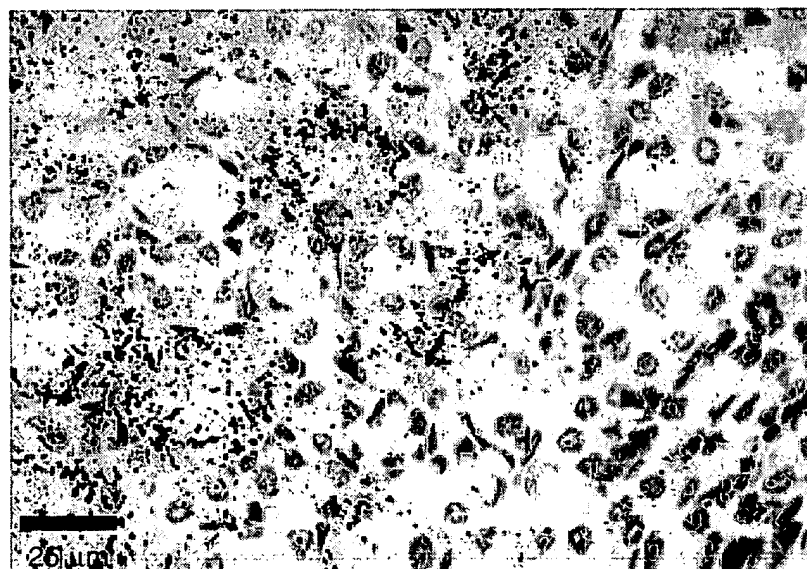
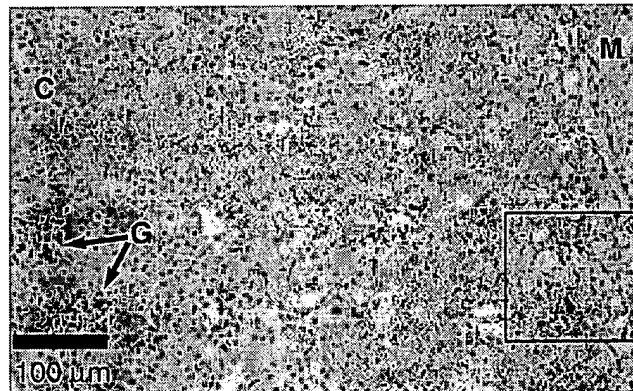
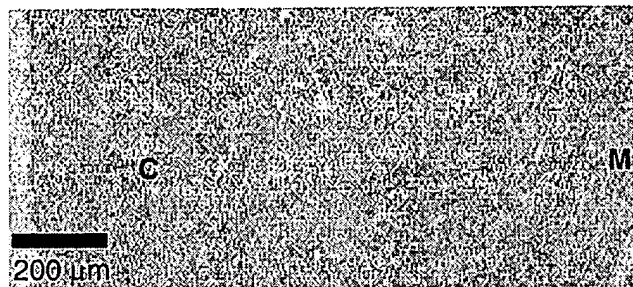
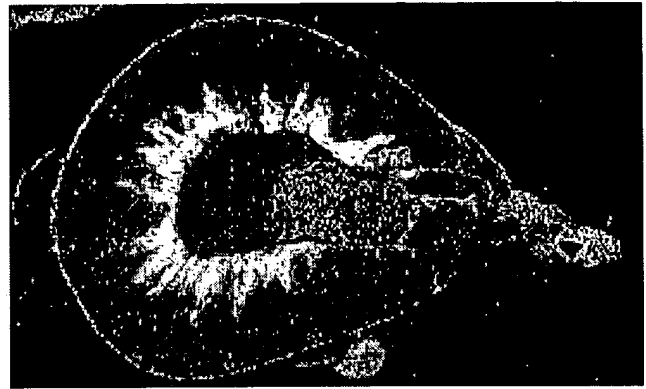
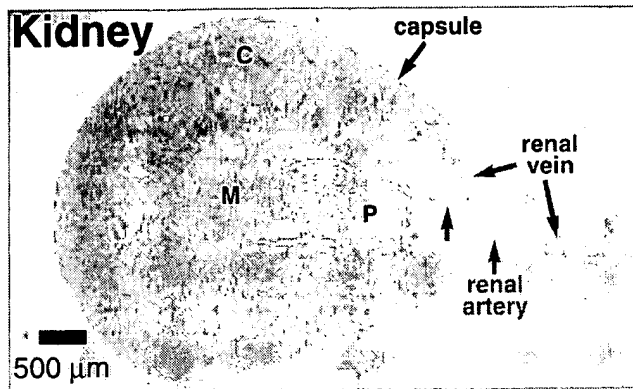
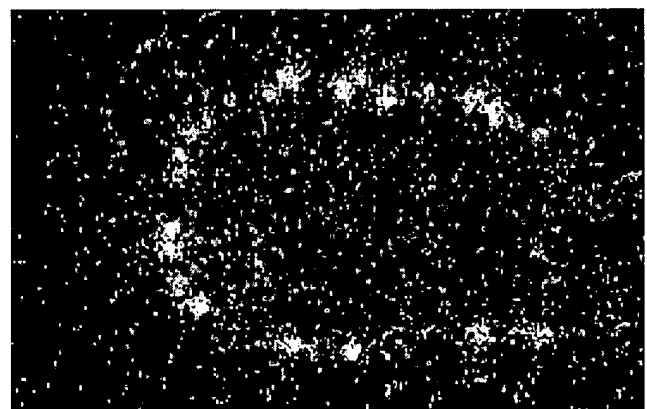
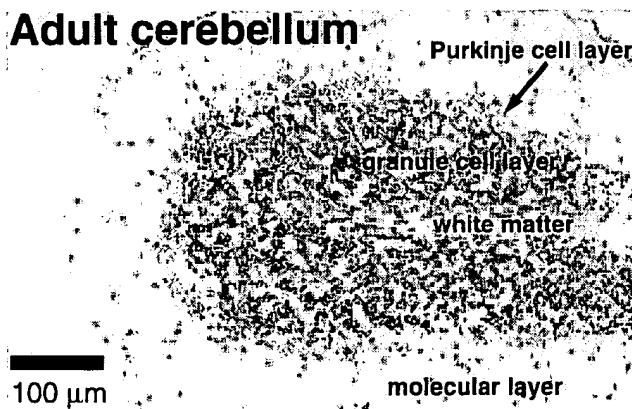
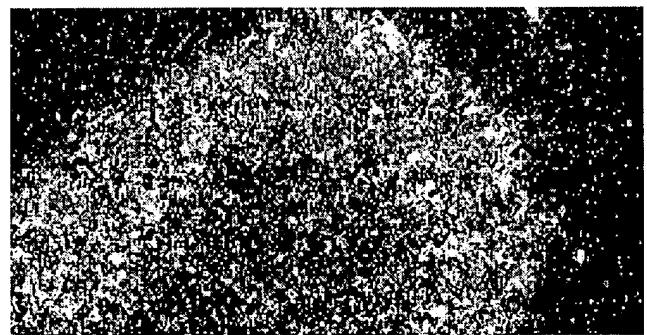
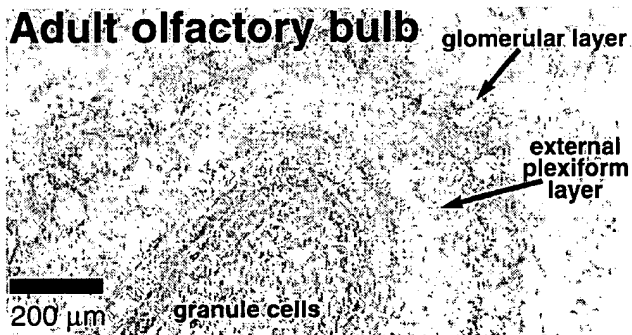
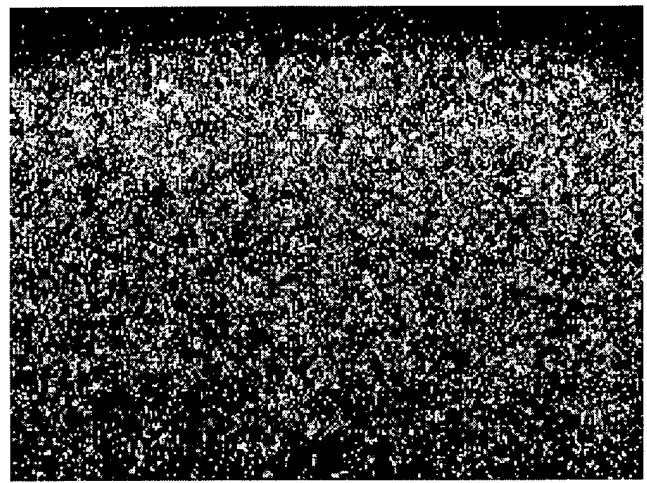
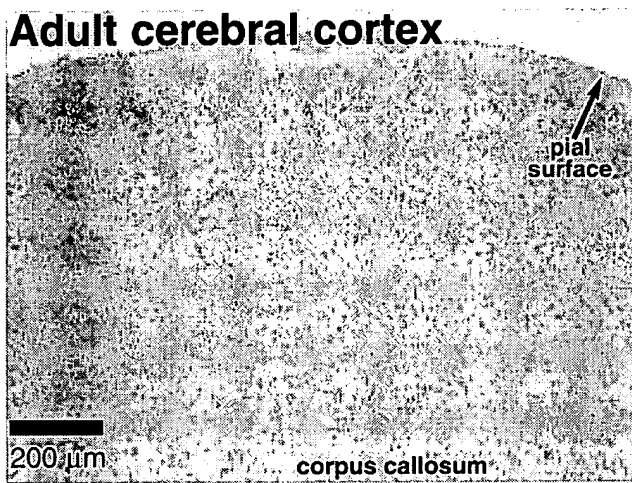
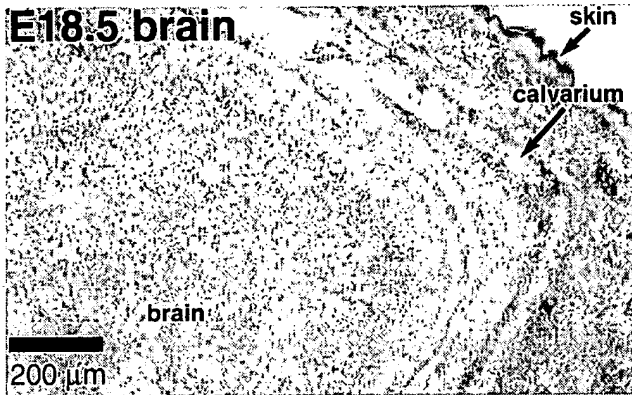


FIG. 12



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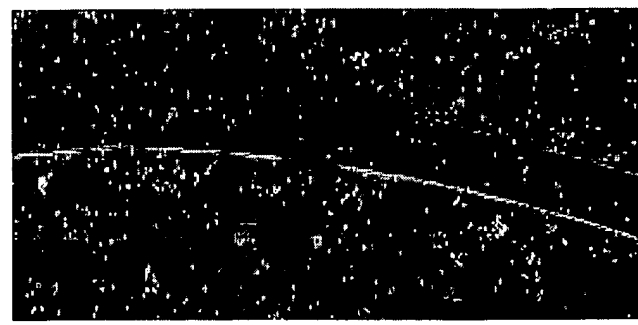
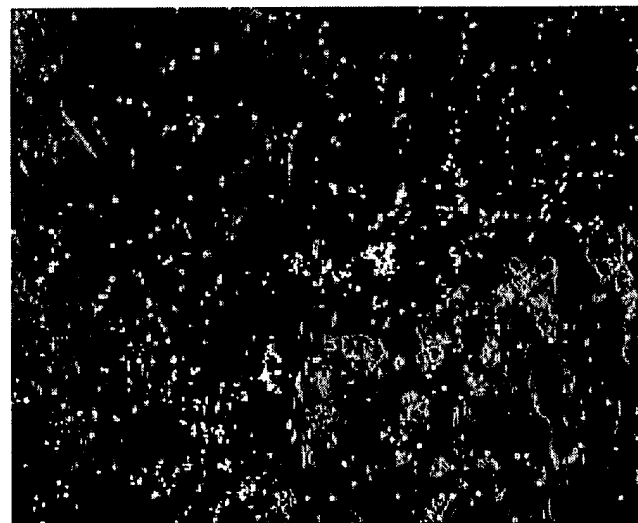
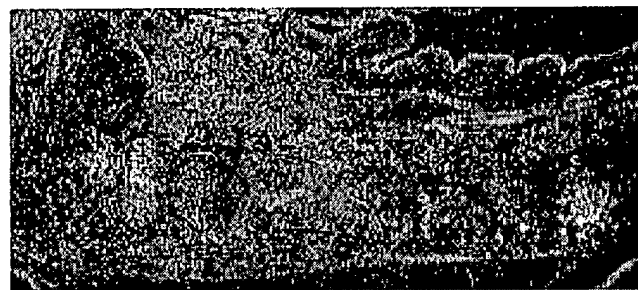
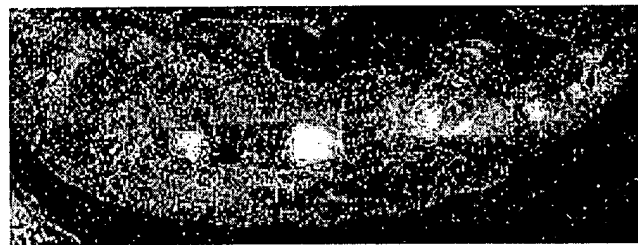
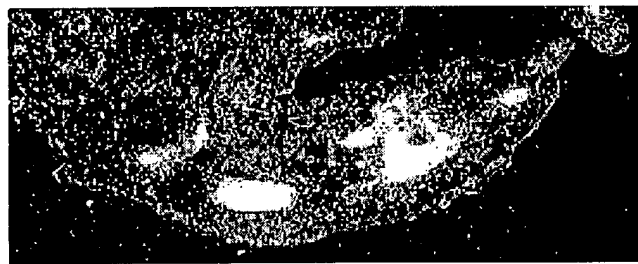


FIG. 14A

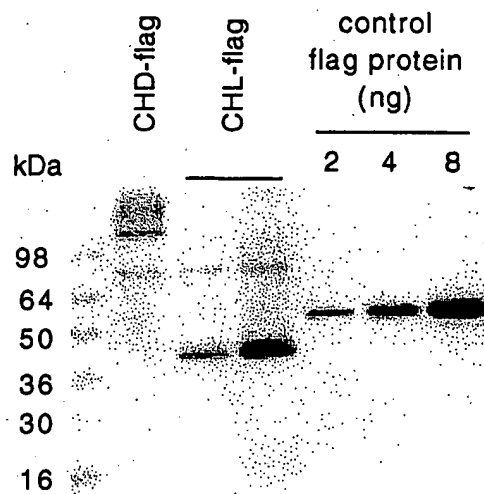


FIG. 14B

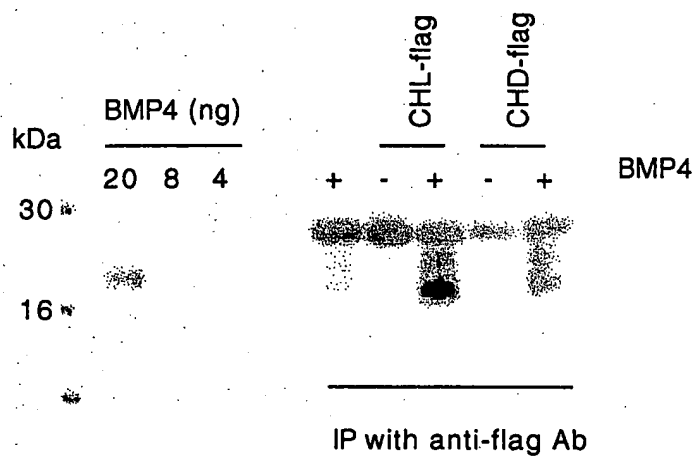


FIG. 14C

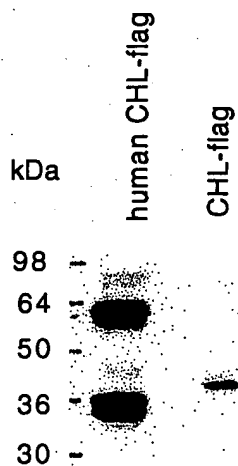
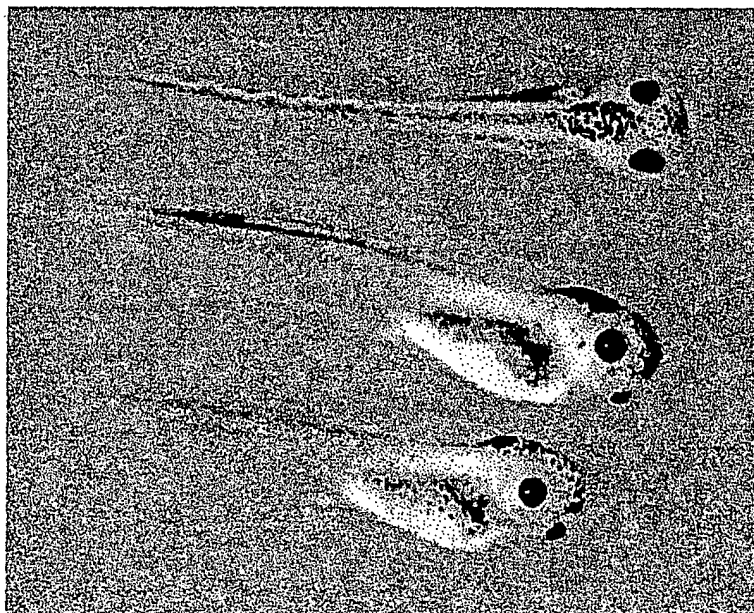


FIG. 15A



FIG. 15B



000001" 5.010260

FIG. 16

Inhibitory effect of CHL on the BMP4-dependent erythrocyte generation from ES cells in 7 days

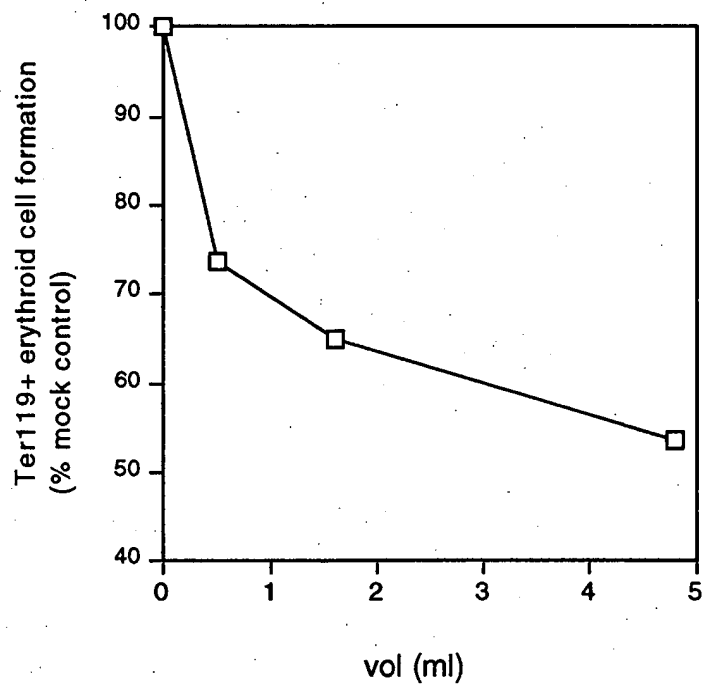


FIG. 17

BMP-4 titration on Bone Marrow Stromal Cell Line A5-F

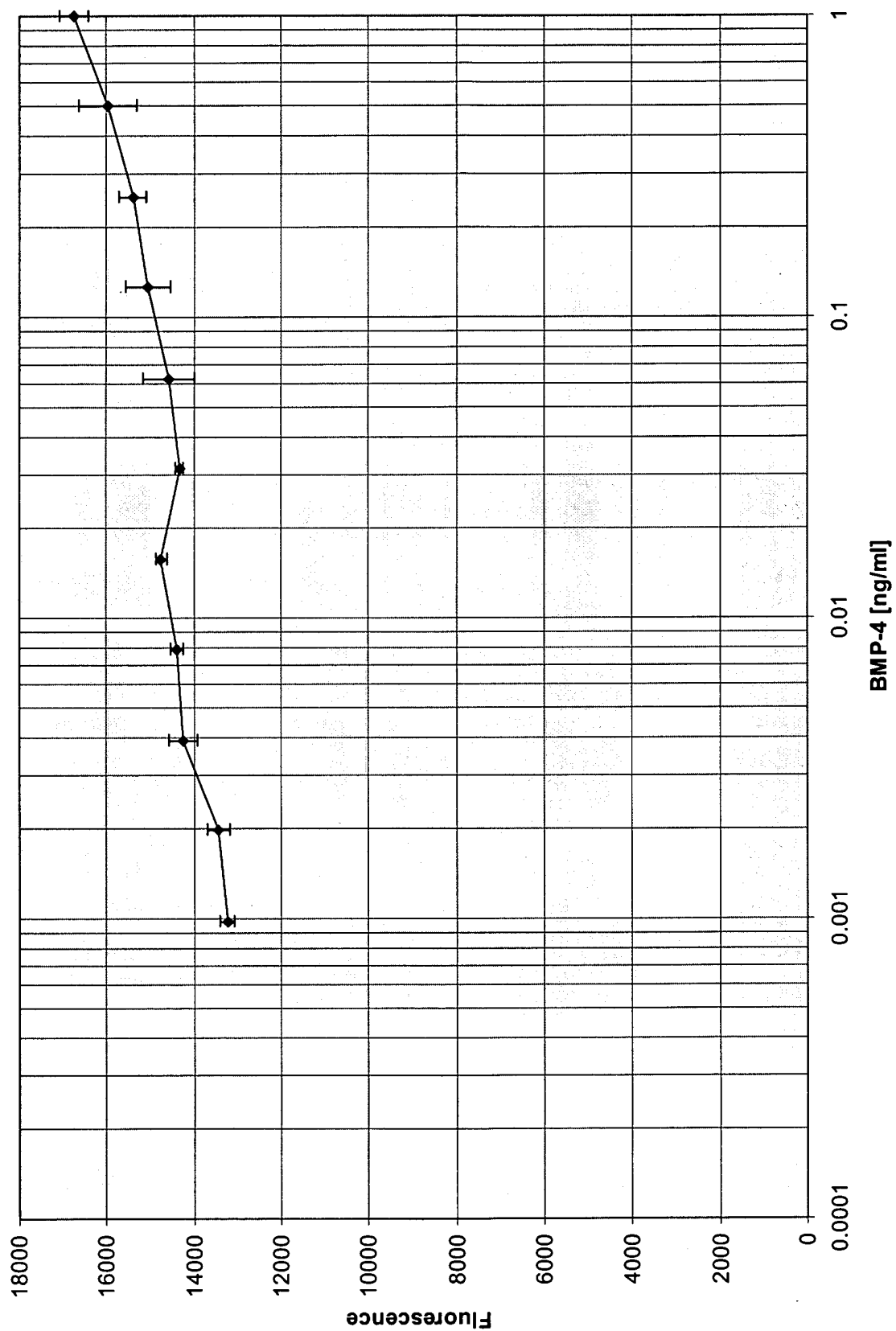


FIG. 18

